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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/459,808A

DATE: 04/06/2000  
TIME: 09:52:57

Input Set: I459808A.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Ashkenazi, Avi J.  
2 <120> TITLE OF INVENTION: APO-2 LIGAND  
3 <130> FILE REFERENCE: 11669.22US03  
4 <140> CURRENT APPLICATION NUMBER: US/09/459,808A  
5 <141> CURRENT FILING DATE: 1999-12-13  
6 <150> EARLIER APPLICATION NUMBER: 08/584,031  
7 <151> EARLIER FILING DATE: 1996-01-09  
8 <160> NUMBER OF SEQ ID NOS: 17  
9 <170> SOFTWARE: PatentIn Ver. 2.0  
10 <210> SEQ ID NO 1  
11 <211> LENGTH: 281  
12 <212> TYPE: PRT  
13 <213> ORGANISM: Homo sapiens  
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15 Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys  
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17 Val Leu Ile Val Ile Phe Thr Val Leu Gln Ser Leu Cys Val Ala  
18 20 25 30  
19 Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys  
20 35 40 45  
21 Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr  
22 50 55 60  
23 Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val  
24 65 70 75 80  
25 Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser  
26 85 90 95  
27 Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro  
28 100 105 110  
29 Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly  
30 115 120 125  
31 Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu  
32 130 135 140  
33 Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly  
34 145 150 155 160  
35 His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile  
36 165 170 175  
37 His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe  
38 180 185 190  
39 Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln  
40 195 200 205  
41 Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys  
42 210 215 220  
43 Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr  
44 225 230 235 240

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45      Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
46                245                250                255
47      Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
48                260                265                270
49      Ser Phe Phe Gly Ala Phe Leu Val Gly
50                275                280
51 <210> SEQ ID NO 2
52 <211> LENGTH: 1042
53 <212> TYPE: DNA
54 <213> ORGANISM: Homo sapiens
55 <400> SEQUENCE: 2
56      tttcctcact gactataaaa gaatagagaa ggaagggcctt cagtgaccgg ctgcctggct 60
57      gacttacagc agtcagactc tgacaggatc atggctatga tggagggtcca ggggggaccc 120
58      agcctgggac agacctgcgt gctgatcgtg atcttcacag tgctcctgca gtctctctgt 180
59      gtggctgtaa cttacgtgta ctttaccacac gagctgaagc agatgcagga caagtactcc 240
60      aaaagtggca ttgcttgitt cttaaaagaa gatgacagtt attgggaccc caatgacgaa 300
61      gagagtatga acagcccctg ctggcaagtc aagtggcaac tccgtcagct cgttagaaag 360
62      atgattttga gaacctctga ggaaaccatt tctacagttc aagaaaagca acaaaaatatt 420
63      tctcccctag tgagagaaaag aggtcctcag agagtagcag ctacacataac tgggaccaga 480
64      ggaagaagca acacattgtc ttctccaaac tccaagaatg aaaaggctct gggccgcaaa 540
65      ataaactcct gggaatcatc aaggagtggg cattcattcc tgagcaactt gcacttgagg 600
66      aatggtgaac tggatcatcca tgaaaaaggg ttttactaca tctattccca aacatacttt 660
67      cgatttcagg aggaaataaaa agaaaacaca aagaacgaca acaaatggt ccaatatatt 720
68      taaaaataca caagttatcc tgaccctata ttggtgatga aaagtgctag aaatagttgt 780
69      tggcttaaaag atgcagaata tggactctat tccatctatc aagggggaat atttgagctt 840
70      aaggaaaatg acagaatttt tgtttctgta acaaatgagc acttgataga catggaccat 900
71      gaagccagtt ttttcggggc ctttttagtt ggctaactga cctggaaaga aaaagcaata 960
72      acctcaaagt gactattcag ttttcaggat gatacactat gaagatgttt caaaaaatct 1020
73      gaccaaaca acaaacaga aa                                1042
74 <210> SEQ ID NO 3
75 <211> LENGTH: 390
76 <212> TYPE: DNA
77 <213> ORGANISM: Homo sapiens
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79      gggaccccaa tgacgaagag agtatgaaca gcccctgctg gcaagtcaag tggcaactcc 60
80      gtcagctcgt tagaaagatg attttgagaa cctctgagga aaccatttct acagttcaag 120
81      aaaagcaaca aaatatttct cccctagtga gagaaagagg tcctcagaga gtagcagctc 180
82      acataactgg gaccagagga agaagcaaca cattgtcttc tccaaactcc aagaatgaaa 240
83      aggctctggg ccgcaaaata aactcctggg aatcatcaag gagtgggcat tcattcctga 300
84      gcaacttgca cttgaggaat ggtgaactgg tcatccatga aaaagggttt tactacatct 360
85      attcccaaac atactttcga tttcaggagg                                390
86 <210> SEQ ID NO 4
87 <211> LENGTH: 60
88 <212> TYPE: DNA
89 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <221> NAME/KEY: misc_feature
92 <222> LOCATION: (1)..(60)
93 <223> OTHER INFORMATION: Sequence is synthesized
94 <400> SEQUENCE: 4
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97      <211> LENGTH: 60
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99      <213> ORGANISM: Artificial Sequence
100     <220> FEATURE:
101     <221> NAME/KEY: misc_feature
102     <222> LOCATION: (1)..(60)
103     <223> OTHER INFORMATION: Sequence is synthesized
104     <400> SEQUENCE: 5
105     ggtgaactgg tcatccatga aaaaggggtt tactacatct attcccaaac atacttttcga 60
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107     <211> LENGTH: 13
108     <212> TYPE: PRT
109     <213> ORGANISM: Artificial Sequence
110     <220> FEATURE:
111     <221> NAME/KEY: UNSURE
112     <222> LOCATION: (1)..(13)
113     <223> OTHER INFORMATION: Sequence is synthesized
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116     1             5             10
117     <210> SEQ ID NO 7
118     <211> LENGTH: 27
119     <212> TYPE: PRT
120     <213> ORGANISM: Artificial Sequence
121     <220> FEATURE:
122     <221> NAME/KEY: UNSURE
123     <222> LOCATION: (1)..(27)
124     <223> OTHER INFORMATION: Sequence is synthesized
125     <400> SEQUENCE: 7
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128     Phe Arg Gly Lys Asp Leu Pro Val Leu Asp Gln
129     20             25
130     <210> SEQ ID NO 8
131     <211> LENGTH: 24
132     <212> TYPE: PRT
133     <213> ORGANISM: Artificial Sequence
134     <220> FEATURE:
135     <221> NAME/KEY: UNSURE
136     <222> LOCATION: (1)..(24)
137     <223> OTHER INFORMATION: Sequence is synthesized
138     <400> SEQUENCE: 8
139     Met Gly His His His His His His His His His Ser Ser Gly His
140     1             5             10             15
141     Ile Asp Asp Asp Asp Lys His Met
142     20
143     <210> SEQ ID NO 9
144     <211> LENGTH: 175
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145 <212> TYPE: PRT
146 <213> ORGANISM: Homo sapiens
147 <400> SEQUENCE: 9
148   Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
149       1             5             10             15
150   Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
151             20             25             30
152   Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
153             35             40             45
154   Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
155             50             55             60
156   Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
157             65             70             75             80
158   Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
159             85             90             95
160   Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
161             100            105            110
162   Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
163             115            120            125
164   Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
165             130            135            140
166   His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
167             145            150            155            160
168   Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
169             165            170            175
170 <210> SEQ ID NO 10
171 <211> LENGTH: 132
172 <212> TYPE: PRT
173 <213> ORGANISM: Homo sapiens
174 <400> SEQUENCE: 10
175   Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe Thr
176       1             5             10             15
177   Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu Asp
178             20             25             30
179   Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp Gly
180             35             40             45
181   Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asn Ile
182             50             55             60
183   Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys Lys
184             65             70             75             80
185   Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys Asp
186             85             90             95
187   Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp Phe
188             100            105            110
189   His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly Glu
190             115            120            125
191   Phe Cys Val Leu
192             130
193 <210> SEQ ID NO 11
194 <211> LENGTH: 151

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196 <213> ORGANISM: Homo sapiens
197 <400> SEQUENCE: 11
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199       1             5             10             15
200   Gln Leu Asn His Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln
201               20             25             30
202   Gly Gly Pro Ala Leu Gly Arg Ser Phe Leu His Gly Pro Glu Leu Asp
203           35             40             45
204   Lys Gly Gln Leu Arg Ile His Arg Asp Gly Ile Tyr Met Val His Ile
205       50             55             60
206   Gln Val Thr Leu Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His
207       65             70             75             80
208   Pro Thr Thr Leu Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile
209               85             90             95
210   Ser Leu Leu Arg Leu Ser Phe His Phe His Gln Gly Cys Thr Ile Val
211               100            105            110
212   Ser Gln Arg Leu Thr Pro Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn
213           115            120            125
214   Leu Thr Gly Thr Leu Leu Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe
215       130            135            140
216   Gly Val Gln Trp Val Arg Pro
217       145            150
218 <210> SEQ ID NO 12
219 <211> LENGTH: 148
220 <212> TYPE: PRT
221 <213> ORGANISM: Homo sapiens
222 <400> SEQUENCE: 12
223   Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys Lys Ser Trp Ala Tyr Leu
224       1             5             10             15
225   Gln Val Ala Lys His Leu Asn Lys Thr Lys Leu Ser Trp Asn Lys Asp
226               20             25             30
227   Gly Ile Leu His Gly Val Arg Tyr Gln Asp Gly Asn Leu Val Ile Gln
228           35             40             45
229   Phe Pro Gly Leu Tyr Phe Ile Cys Gln Leu Gln Phe Leu Val Gln
230       50             55             60
231   Cys Pro Asn Asn Ser Val Asp Leu Lys Leu Glu Leu Leu Ile Asn Lys
232       65             70             75             80
233   His Ile Lys Lys Gln Ala Leu Val Thr Val Cys Glu Ser Gly Met Gln
234           85             90             95
235   Thr Lys His Val Tyr Gln Asn Leu Ser Gln Phe Leu Leu Asp Tyr Leu
236       100            105            110
237   Gln Val Asn Thr Thr Ile Ser Val Asn Val Asp Thr Phe Gln Tyr Ile
238           115            120            125
239   Asp Thr Ser Thr Phe Pro Leu Glu Asn Val Leu Ser Ile Phe Leu Tyr
240       130            135            140
241   Ser Asn Ser Asp
242       145
243 <210> SEQ ID NO 13
244 <211> LENGTH: 157
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**VERIFICATION SUMMARY**  
**PATENT APPLICATION US/09/459,808A**

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Line ? Error/Warning

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